

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/269,118ADATE: 12/20/95  
TIME: 16:22:17

INPUT SET: S14548.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

## (1) General Information:

(i) APPLICANT: Inouye, Sumiko  
Hsu, Mei-Yin  
Eagle, Susan  
Inouye, Masayori

(ii) TITLE OF INVENTION: Prokaryotic Reverse Transcriptase

(iii) NUMBER OF SEQUENCES: 45

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Weiser & Associates  
(B) STREET: 230 South Fifteenth Street, Suite 500  
(C) CITY: Philadelphia  
(D) STATE: Pennsylvania  
(E) COUNTRY: U.S.A.  
(F) ZIP: 19102

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/269,118  
(B) FILING DATE: 30-JUN-1994  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Weiser, Gerard J.  
(B) REGISTRATION NUMBER: 19,763  
(C) REFERENCE/DOCKET NUMBER: 377.5888P

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 215-875-8383  
(B) TELEFAX: 215-875-8394

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2176 base pairs

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/269,118A

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47 (B) TYPE: nucleic acid  
48 (C) STRANDEDNESS: double  
49 (D) TOPOLOGY: linear  
50  
51

52 (ix) FEATURE:

53 (A) NAME/KEY: CDS  
54 (B) LOCATION: 640..2094  
55  
56

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

58	TCATCCGCGC GGACACCCCC TCCTACGTGC CCCCCGACGC GGAGAGCGGC GTGGAGACGG	60
59	TGTACCGCGT TTCCCTGGAT GGTCACCTGG TGGCGGTGGA GTGGGGCCCG CGCACGGGCT	120
60	CGCCGCGTCA CCAGCGGCTC TGGTTCGACT CGGATGCGGA AGCCCCCGGA GCCTACTTCG	180
61	CGCGCCTCGA GAAGTTGGCG GCTGACGGCT ACATCGACGC GGCTTCGGCA TTGGTCTAAA	240
62	CCCTTCAACC ACGGCTCGGC CGCCACGCGC GGCCGGCAGG ACAGGTGCGA CGAACAGACG	300
63	ACGACGTGCG CTTCACGCGC GAGCAGCCGA GAGAGGTCCG GAGTGCATCA GCCTGAGCGC	360
64	CTCGAGCGGC GGAGCGGCGT TGCGCCGCTC CGGTTGGAAT GCAGGACACT CTCCGCAAGG	420
65	TAGCCTGTTT TTGGCTCTCT CCCTCCTAGG CACTACGGCC AGGGTGGGTA GCGGAGCCAA	480
66	CGACGCCACC GCCGTTTACC CACCCCGGCC GTAGTGCCTA GGAGGGGAGA GCCGGTGAGG	540
67	CTACCGTGCC CCAGGTAAGA TGGTGGTGCT TTCCCGGCCT CCGTCGACTG CTCGCGCCAT	600
68	GTCCCGTCTT CCATCGCCGC GCCCGCCCAA GGTGCAGAC ATG ACC GCC AGG CTG	654
69		Met Thr Ala Arg Leu
70		1 5
71	GAC CCG TTC GTC CCC GCA GCT TCG CCG CAG GCC GTG CCC ACG CCC GAG	702
72	Asp Pro Phe Val Pro Ala Ala Ser Pro Gln Ala Val Pro Thr Pro Glu	
73		10 15 20
74	CTC ACC GCT CCG TCG TCA GAC GCG GCC GCG AAG CGT GAA GCC CGC CGG	750
75	Leu Thr Ala Pro Ser Ser Asp Ala Ala Ala Lys Arg Glu Ala Arg Arg	
76		25 30 35
77	CTC GCG CAC GAA GCG TTG CTC GTC CGC GCG AAG GCC ATC GAC GAA GCG	798
78	Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys Ala Ile Asp Glu Ala	
79		40 45 50
80	GGC GGC GCC GAC GAC TGG GTG CAG GCG CAG CTC GTC TCC AAG GGG CTC	846
81	Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu Val Ser Lys Gly Leu	
82		55 60 65
83	GCG GTC GAG GAC CTG GAC TTC TCC AGC GCC TCC GAG AAG GAC AAG AAG	894

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/269,113A

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100	Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser Glu Lys Asp Lys Lys	
101	70 75 80 85	
102		
103	GCC TGG AAG GAG AAG AAG AAG GCC GAG GCC ACC GAG CGC CGC GCG CTG	942
104	Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr Glu Arg Arg Ala Leu	
105	90 95 100	
106		
107	AAG CGT CAG GCG CAC GAG GCG TGG AAG GCC ACG CAC GTG GGC CAC CTG	990
108	Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr His Val Gly His Leu	
109	105 110 115	
110		
111	GGC GCG GGC GTG CAC TGG GCG GAG GAC CGC CTG GCC GAC GCG TTC GAC	1038
112	Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu Ala Asp Ala Phe Asp	
113	120 125 130	
114		
115	GTG CCC CAC CGC GAG GAG CGC GCC CGG GCC AAC GGC CTG ACG GAG CTG	1086
116	Val Pro His Arg Glu Glu Arg Ala Arg Ala Asn Gly Leu Thr Glu Leu	
117	135 140 145	
118		
119	GAC TCC GCG GAG GCG CTG GCC AAG GCG CTG GGG CTG AGC GTC TCC AAG	1134
120	Asp Ser Ala Glu Ala Leu Ala Lys Ala Leu Gly Leu Ser Val Ser Lys	
121	150 155 160 165	
122		
123	CTC CGC TGG TTC GCG TTC CAC CGG GAG GTC GAC ACG GCC ACG CAC TAC	1182
124	Leu Arg Trp Phe Ala Phe His Arg Glu Val Asp Thr Ala Thr His Tyr	
125	170 175 180	
126		
127	GTG AGC TGG ACC ATT CCG AAG CGG GAC GGC AGC AAG CGC ACG ATT ACG	1230
128	Val Ser Trp Thr Ile Pro Lys Arg Asp Gly Ser Lys Arg Thr Ile Thr	
129	185 190 195	
130		
131	TCC CCC AAG CCT GAG CTG AAG GCA GCG CAG CGC TGG GTG CTG TCC AAC	1278
132	Ser Pro Lys Pro Glu Leu Lys Ala Ala Gln Arg Trp Val Leu Ser Asn	
133	200 205 210	
134		
135	GTC GTG GAG CGG CTG CCG GTC CAC GGC GCC GCC CAC GGC TTC GTG GCG	1326
136	Val Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala	
137	215 220 225	
138		
139	GGA CGC TCC ATC CTC ACC AAC GCG CTG GCC CAC CAG GGC GCG GAC GTC	1374
140	Gly Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val	
141	230 235 240 245	
142		
143	GTG GTC AAG GTG GAC CTC AAG GAC TTC TTC CCC TCC GTC ACC TGG CGC	1422
144	Val Val Lys Val Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Trp Arg	
145	250 255 260	
146		
147	CGG GTG AAG GGC CTG TTG CGC AAG GGC GGC CTG CGG GAG GGC ACG TCC	1470
148	Arg Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Arg Glu Gly Thr Ser	
149	265 270 275	
150		
151	ACG CTG CTG TCC CTC CTC TCC ACG GAA GCG CCG CGG GAG GCG GTC CAG	1518
152	Thr Leu Leu Ser Leu Leu Ser Thr Glu Ala Pro Arg Glu Ala Val Gln	

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	280	285	290	
153				
154				
155	TTC CGC GGC AAG CTC CTG CAC GTC GCC AAG GGC CCG CGC GCC CTG CCC			1566
156	Phe Arg Gly Lys Leu Leu His Val Ala Lys Gly Pro Arg Ala Leu Pro			
157	295	300	305	
158				
159	CAG GGC GCC CCC ACG TCG CCC GGC ATC ACC AAC GCG CTC TGC CTG AAG			1614
160	Gln Gly Ala Pro Thr Ser Pro Gly Ile Thr Asn Ala Leu Cys Leu Lys			
161	310	315	320	325
162				
163	CTC GAC AAG CGG CTG TCC GCC CTC GCG AAG CGG CTG GGC TTC ACC TAC			1662
164	Leu Asp Lys Arg Leu Ser Ala Leu Ala Lys Arg Leu Gly Phe Thr Tyr			
165		330	335	340
166				
167	ACG CGC TAC GCG GAC GAC CTG ACC TTC TCC TGG ACG AAG GCG AAG CAG			1710
168	Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Thr Lys Ala Lys Gln			
169		345	350	355
170				
171	CCC AAG CCG CGG CGG ACG CAG CGT CCC CCC GTC GCG GTC CTC CTG TCT			1758
172	Pro Lys Pro Arg Arg Thr Gln Arg Pro Pro Val Ala Val Leu Leu Ser			
173		360	365	370
174				
175	CGC GTC CAG GAA GTG GTG GAG GCG GAG GGC TTC CGC GTG CAC CCG GAC			1806
176	Arg Val Gln Glu Val Val Glu Ala Glu Gly Phe Arg Val His Pro Asp			
177		375	380	385
178				
179	AAG ACG CGC GTC GCC CGC AAG GGC ACG CGG CAG CGG GTC ACC GGG CTC			1854
180	Lys Thr Arg Val Ala Arg Lys Gly Thr Arg Gln Arg Val Thr Gly Leu			
181	390	395	400	405
182				
183	GTC GTG AAT GCG GCG GGC AAG GAC GCG CCC GCG GCC CGA GTC CCG CGC			1902
184	Val Val Asn Ala Ala Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg			
185		410	415	420
186				
187	GAC GTC GTC CGC CAG CTC CGC GCC GCC ATC CAC AAC CGG AAG AAG GGC			1950
188	Asp Val Val Arg Gln Leu Arg Ala Ala Ile His Asn Arg Lys Lys Gly			
189		425	430	435
190				
191	AAG CCG GGC CGC GAG GGC GAG TCG CTC GAG CAG CTC AAG GGC ATG GCC			1998
192	Lys Pro Gly Arg Glu Gly Glu Ser Leu Glu Gln Leu Lys Gly Met Ala			
193		440	445	450
194				
195	GCC TTC ATC CAC ATG ACG GAC CCG GCC AAG GGC CGC GCC TTC CTG GCT			2046
196	Ala Phe Ile His Met Thr Asp Pro Ala Lys Gly Arg Ala Phe Leu Ala			
197		455	460	465
198				
199	CAG CTC ACG GAG CTC GAG TCC ACG GCG AGC GCC GCT CCG CAG GCG GAG			2094
200	Gln Leu Thr Glu Leu Glu Ser Thr Ala Ser Ala Ala Pro Gln Ala Glu			
201	470	475	480	485
202				
203	TGACGCTCAG CGCGCGTCCG TCGCCGACGT GCCGCGCGCC AGCAACGCCG CATTCAGCAA			2154
204				
205	CTCCGTCAGC CGGCGCGGGT AC			2176

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206  
207  
208 (2) INFORMATION FOR SEQ ID NO:2:  
209  
210 (i) SEQUENCE CHARACTERISTICS:  
211 (A) LENGTH: 263 amino acids  
212 (B) TYPE: amino acid  
213 (D) TOPOLOGY: linear  
214  
215 (ii) MOLECULE TYPE: protein  
216  
217  
218  
219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
220  
221 Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro  
222 1 5 10 15  
223  
224 Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met  
225 20 25 30  
226  
227 Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn  
228 35 40 45  
229  
230 Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys  
231 50 55 60  
232  
233 Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu  
234 65 70 75 80  
235  
236 Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser  
237 85 90 95  
238  
239 Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp  
240 100 105 110  
241  
242 Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn  
243 115 120 125  
244  
245 Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp  
246 130 135 140  
247  
248 Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu  
249 145 150 155 160  
250  
251 Pro Phe Lys Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp  
252 165 170 175  
253  
254 Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys  
255 180 185 190  
256  
257 Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro  
258 195 200 205